

Figure 1A
CTGF-4

1 CGGACTTTACCCAGCTCCACTGGAGGACACCTCCTCAGCCCCCAATTCTGCAAGTGGC 60
1 D F T P A P L E D T S S R P Q F C K W P 20

61 CATGTGAGTGGCCGCGCATCCCCACCCGCTGCCGCTGGGGGTGAGCCTCATCACAGATG 120
21 C E C P P S P P R C P L G V S L I T D G 40

121 GCTGTGAGTGTCTAAGATGTGCGCTCAGCAGCTTGGGGACAACCTGCACGGAGGCTGCCA 180
41 C E C C K M C A Q Q L G D N C T E A A I 60

181 TCTGTGACCCCAACGGGGCTCTACTGTGACTACAGCGGGACCGCCGAGGTACGCAA 240
61 C D P H R G L Y C D Y S G D R P R Y A I 80

241 TAGGAGTGTGTGCACAGGTGGTTCGGTGTGGGCTGCGTCCTGGATGGGGTGCGCTACAACA 300
81 G V C A Q V V G V G C V L D G V R Y N N 100

301 ACGGCCAGTCTCTCCAGCCTAAGTACAACCTGCACGTGCATCGACGGCGCGGTGG 360
101 G Q S F Q P N C K Y N C T C I D G A V G 120

361 GCTGCACACCACTGTGCCTCCGAGTGCACCCCCCGCTCTCTGGTGGCCCCACCCGCGGC 420
121 C T P L C L R V R P P R L W C P H P R R 140

421 GCGTGAGCATACCTGGCCACTGCTGTGAGCAGTGGGTATGTGAGGACGACCCAAGAGGC 480
141 V S I P G H C C E Q W V C E D D A K R P 160

481 CACGCAAGACCGCACCCCGTGACACAGGAGCCTTCGATGCTGTGGGTGAGGTGGAGGCAT 540
161 R K T A P R D T G A F D A V G E V E A W 180

541 GGCACAGGAACCTGCATAGCCTACACAAGCCCTGGAGCCCTTGCTCCACCACTGCGGCC 600
181 H R N C I A Y T S P W S P C S T S C G L 200

601 TGGGGTCTCCACTCGGATCTCCAATGTTAAGCCCCAGTGTGCTGAGCAAGAGAGCC 660
201 G V S T R I S N V N A Q C W P E Q E S R 220

661 GCCTCTGCAACTTGGCGCCATGCGATGTGGACATCCATACACTCATTAAGGCAGGAAGA 720
221 L C N L R P C D V D I H T L I K A G K K 240

721 AGTGTCTGGCTGTGTACCAGCCAGAGGCATCCATGAACCTTACACTTGGCGGCTGCATCA 780
241 C L A V Y Q P E A S M N F T L A G C I S 260

781 GCACACGCTCCTATCAACCCAAGTACTGTGGAGTTTGCATGGACAATAGGTGCTGCATCC 840
261 T R S Y Q P K Y C G V C M D N R C C I P 280

841 CCTACAAGTCTAAGACTATCGACGTGTCCTTCCAGTGTCTGATGGGCTTGGCTTCTCCC 900
281 Y K S K T I D V S F Q C P D G L G F S R 300

901 GCCAGGTCTATGGATTAATGCCTGCTTCTGTAACCTGAGCTGTAGGAATCCCAATGACA 960
301 Q V L W I N A C F C N L S C R N P N D I 320

961 TCTTTGCTGACTTGAATCCTACCCTGACTTCTCAGAAATTGCCAACTAGGCAGGCACAA 1020
321 F A D L E S Y P D F S E I A N * 335

1021 ATCTTGGGTCTTGGGGACTAACCAATGCCTGTGAAGCAGTCAGCCCTTATGGCCAATAA 1080

1081 CTTTTCACCAATGAGCCTTAGTTACCCTGATCTGGACCTTGGCCTCCATTCTGTCTCT 1140

IGF-Binding
Domain

vonWillebrand
Factor Type C
Repeat

Sulfated
Glycoconjugate
Binding Motif

C-Terminal
Dimerization &
Receptor-Binding
Domain

Figure 1B
CTGF-4

1141	AACCATTCAAATGACGCCTGATGGTGCTGCTCAGGCCCATGCTATGAGTTTCTCCTTGA	1200
1201	TATCATTACAGCATCTACTCTAAAGAAAAATGCCTGTCTCTAGCTGTTCTGGACTACACCC	1260
1261	AAGCCTGATCCAGCCTTTCCAAGTCACTAGAAGTCCTGCTGGATCTTGCCTAAATCCCAA	1320
1321	GAAATGGAATCAGGTAGACTTTTAATATCACTAATTTCTTCTTTAGATGCCAAACCACAA	1380
1381	GACTCTTTGGGTCCATTGAGATGAATAGATGGAATTTGGAACAATAGAATAATCTATTAT	1440
1441	TTGGAGCCTGCCAAGAGGTACTGTAATGGGTAATTCTGACGTCAGCGCACCAAACTATC	1500
1501	CTGATTCCAAATATGTATGCACCTCAAGGTCATCAAAACATTTGCCAAGTGAGTTGAATAG	1560
1561	TTGCTTAATTTTGATTTTAAATGGAAGTTGTATCCATTAACTGGGCATTGTTGAGGTT	1620
1621	AAGTTTCTCTTCACCCCTACACTGTGAAGGGTACAGATTAGGTTTGTCCCAGTCAGAAAT	1680
1681	AAAATTTGATAAACATTCTGTGATGGGAAAAGCCCCAGTTAATACTCCAGAGACAGG	1740
1741	GAAAGGTCAGCCCATTTCAGAAGGACCAATTGACTCTCAGCTGAATCAGCTGCTGACTG	1800
1801	GCAGGGCTTTGGGCAGTTGGCCAGGCTCTTCTTGAATCTTCTCCCTTGCTCTGCTGGG	1860
1861	GTTCATAGGAATTGGTAAGGCCTCTGGACTGGCCTGTCTGGCCCCTGAGAGTGGTGCCCT	1920
1921	GGAACACTCCTCTACTCTTACAGAGCCTTGAGAGACCCAGCTGCAGACCATGCCAGACCC	1980
1981	ACTGAAATGACCAAGACAGGTTTCAGGTAGGGGTGTGGGTCAAACCAAGAAGTGGGTGCC	2040
2041	TTGGTAGCAGCCTGGGGTGACCTCTAGAGCTGGAGGCTGTGGGACTCCAGGGGCCCCCGT	2100
2101	G TTCAGGACACATCTATTGCAGAGACTCATTTACAGCCTTTCGTTCTGCTGACCAAATG	2160
2161	GCCAGTTTTCTGGTAGGAAGATGGAGGTTTACCAGTTGTTTAGAAACAGAAATAGACTTA	2220
2221	ATAAAGGTTTAAAGCTGAAGAGGTTGAAGCTAAAAGGAAAAGGTTGTGTTAATGAATAT	2280
2281	CAGGCTATTATTTATTGTATTAGGAAAATATAATATTTACTGTTAGAAATCTTTTATTTA	2340
2341	GGGCCTTTTCTGTGCCAGACATTGCTCTCAGTGCTTTGCATGTATTAGCTCACTGAATCT	2400
2401	TCACGACAATGTTGAGAAGTTCCCATTTATTATTTCTGTTCTTACAAATGTGAAACGGAAG	2460
2461	CTCATAGAGGTGAGAAAACCAACCAGAGTCACCCAGTTGGTGACTGGGAAAGTTAGGAT	2520
2521	TCAGATCGAAATTGGACTGTCTTTATAACCCATATTTCCCCCTGTTTTTAGAGCTTCCA	2580
2581	AATGTGTCAGAATAGGAAAACATTGCAATAAATGGCTTGATTTTTTAATGTCATTTTTCC	2640

Figure 1C
CTGF-4

2641 CTCTTATAGTCTTTCTAGCTCCTTTTCAAAAGACGAGAATATCTGATTTTCTGATAATT 2700

2701 AGGTGCTTAAGCATCCAAAATACATGGGACACACAAAATCCAGGAATCCCCTGTAGCTT 2760

2761 ATTCCCTCTTTCCCATCGGAACCAGCTCTCATCACACATTTAAAGATGATTCTGTTTAC 2820

2821 CCAATGCTGCATATTGAATGTTGTGTAGTTATTCACAGGGAATTCTGTGCAGTGTGCAGA 2880

2881 GAGATTCTTAAACGGGAAAAGGACTGGGAATACATCCTCCTTACTGTGACCTCCCCAAA 2940

2941 CCTAGTCCAGTGCAAGGTATACAGTGGTGCTCATTAATACTTGATGAATACAGGAAGCT 3000

3001 GTGCATGTGTTCTTACTTTTTATTCTGAAGCTCTCTTCTTCCAAAGCTACATGAAAATAGAA 3060

3061 TTTTAACAGTCAAAATTTTATATTAAGTGTCTTAGCAAAAGAGACATTTAATATTTCAA 3120

3121 GAAATGCATATGTATGTATACATATATTTGTGTATGCGTATGCAAGAATTCTTGATATA 3180

3181 GAGAATTCACCTCCATGAATGATCTCTTCTGTAAGTCAGTGTGAATCATGTTAGATTTTCT 3240

3241 GAGAGTGAAAACACCTGCCATCTACAAATTACAAGGCTGGATAACAGCTCACTCCATTG 3300

3301 AAATTCAGTGGAACCCCAAGAGCTAGGTTCTTACTGAATTTGCATCTCAATTTGGGAAAC 3360

3361 TGAACCTAGCTTTCAAAGATCATAGGAAGTCTGGTTGGAGAACTAGGGATTATTCTGGC 3420

3421 AATGGGTGGAGGAAGGTGGTCAGAATAACCCAGTCGCCATTGGTTTTGAGAAACGGAAC 3480

3481 ATCTTATGCAGAGCCCGGAGGGCAAGTCTCAAACCCATGGGTGAAGCCATGGAGAAGGA 3540

3541 AATTTGGATCCAATGTAATGAAGCTCTTTCTAAGTCAGAATTTCCCTGCAATGGTGTGGC 3600

3601 CTGATTCAATAAAAATTAAGAATAATAAATATAATGGAAAAAAAAAAAAAAAAAAAAA 3658

Figure 2A

	10	20	30	
1	- - - - -	- - - - -	- - - - -	HWHGU74P.aa
1	M R W L L P W T L A A V A V L R V G N I L	A T A L S P T P T		MuELM1.aa
1	M T - - - - -	- - - - - A A S M G P - - V R - -		HuCTGF.aa
1	M S - - - - -	- - - - - S R I A R A L A L - - -		HuCyr61.aa
1	M Q - - - - -	- - - - - S V Q S T S F C L R K Q		HuNOV.aa
	40	50	60	
1	- - D F T P A P L E D T S S R P - - -	Q F C K W P C - - E C		HWHGU74P.aa
31	T M T F T P A P L E E T T T R P - - -	E F C K W P C - - E C		MuELM1.aa
11	- - - V A F V V L L A L C S R P A V G	Q N C S G P C - - R C		HuCTGF.aa
12	- - - - - V V T L L H L - T R L A L S - T	C P A A C - - H C		HuCyr61.aa
15	C L C L T F L - L L H L L G Q V A A T	Q R C P P Q C P G R C		HuNOV.aa
	70	80	90	
24	P P S P - P R C P L G V S L I T D G C E	C C K M C A Q Q L G		HWHGU74P.aa
56	P Q S P - P R C P L G V S L I T D G C E	C C K I C A Q Q L G		MuELM1.aa
36	P D E P A P R C P A G V S L V L D G C G C C	R V C A K Q L G		HuCTGF.aa
33	P L E - A P K C A P G V G L V R D G C G C C	K V C A K Q L N		HuCyr61.aa
44	P A T P - P T C A P G V R A V L D G C S C C	L V C A R Q R G		HuNOV.aa
	100	110	120	
53	D N C T E A A I C D P H R G L Y C D Y S G D R P R Y	A I G V		HWHGU74P.aa
85	D N C T E A A I C D P H R G L Y C D Y S G D R P R Y	A I G V		MuELM1.aa
66	E L C T E R D P C D P H K G L F C D F G S P A N R -	K I G V		HuCTGF.aa
62	E D C S K T Q P C D H T K G L E C N F G A S S T A -	L K G I		HuCyr61.aa
73	E S C S D L E P C D E S S G L Y C D R S A D P S N -	Q T G I		HuNOV.aa
	130	140	150	
83	C - A Q V V G V G C V L D G V R Y N N G Q S F Q P N C K Y N			HWHGU74P.aa
115	C - A Q V V G V G C V L D G V R Y T N G E S F Q P N C R Y N			MuELM1.aa
95	C T A K - D G A P C I F G G T V Y R S G E S F Q S S C K Y Q			HuCTGF.aa
91	C R A Q S E G R P C E Y N S R I Y Q N G E S F Q P N C K H Q			HuCyr61.aa
102	C T A V - E G D N C V F D G V I Y R S G E K F Q P S C K F Q			HuNOV.aa
	160	170	180	
112	C T C I D G A V G C T P L C - L R V R P P R L W C P H P R R			HWHGU74P.aa
144	C T C I D G T V G C T P L C - L S P R P P R L W C R Q P R H			MuELM1.aa
124	C T C L D G A V G C M P L C S M D V R L P S P D C P F P R R			HuCTGF.aa
121	C T C I D G A V G C I P L C P Q E L S L P N L G C P N P R L			HuCyr61.aa
131	C T C R D G Q I G C V P R C Q L D V L L P E P N C P A P R K			HuNOV.aa

Figure 2B

		190		200		210																										
141	V	S	I	P	G	H	C	C	E	Q	W	V	C	E	D	D	A	K	R	P	R	-	-	-	-	K	T	A	P	R	HWHGU74P.aa	
173	V	R	V	P	G	Q	C	C	E	Q	W	V	C	D	D	D	A	R	R	P	R	-	-	-	-	Q	T	A	L	L	MuELM1.aa	
154	V	K	L	P	G	K	C	C	E	E	W	V	C	D	E	P	-	-	-	-	-	-	-	-	K	D	Q	T	V	V	G	HuCTGF.aa
151	V	K	V	T	G	Q	C	C	E	E	W	V	C	D	E	D	S	I	K	D	P	M	E	D	Q	D	G	L	L	G	HuCyr61.aa	
161	V	E	V	P	G	E	C	C	E	K	W	I	C	G	P	D	-	-	-	-	-	-	-	-	E	E	D	S	L	G	G	HuNOV.aa

Figure 2C

		370		380		390																									
285	T	I	D	V	S	F	Q	C	P	D	G	L	G	F	S	R	Q	V	L	W	I	N	A	C	F	C	N	L	S	C	HWHGU74P.aa
317	T	I	S	V	D	F	Q	C	P	E	G	P	G	F	S	R	Q	V	L	W	I	N	A	C	F	C	N	L	S	C	MuELM1.aa
300	T	L	P	V	E	F	K	C	P	D	G	E	V	M	K	K	N	M	M	F	I	K	T	C	A	C	H	Y	N	C	HuCTGF.aa
330	T	V	K	M	R	F	R	C	E	D	G	E	T	F	S	K	N	V	M	I	Q	S	C	K	C	N	Y	N	C	HuCyr61.aa	
308	T	I	Q	A	E	F	Q	C	S	P	G	Q	I	V	K	K	P	V	M	V	I	G	T	C	T	C	H	T	N	C	HuNOV.aa
																			</												

285 317 300 330 308

Figure 3
CTGF-4 Protein Analysis

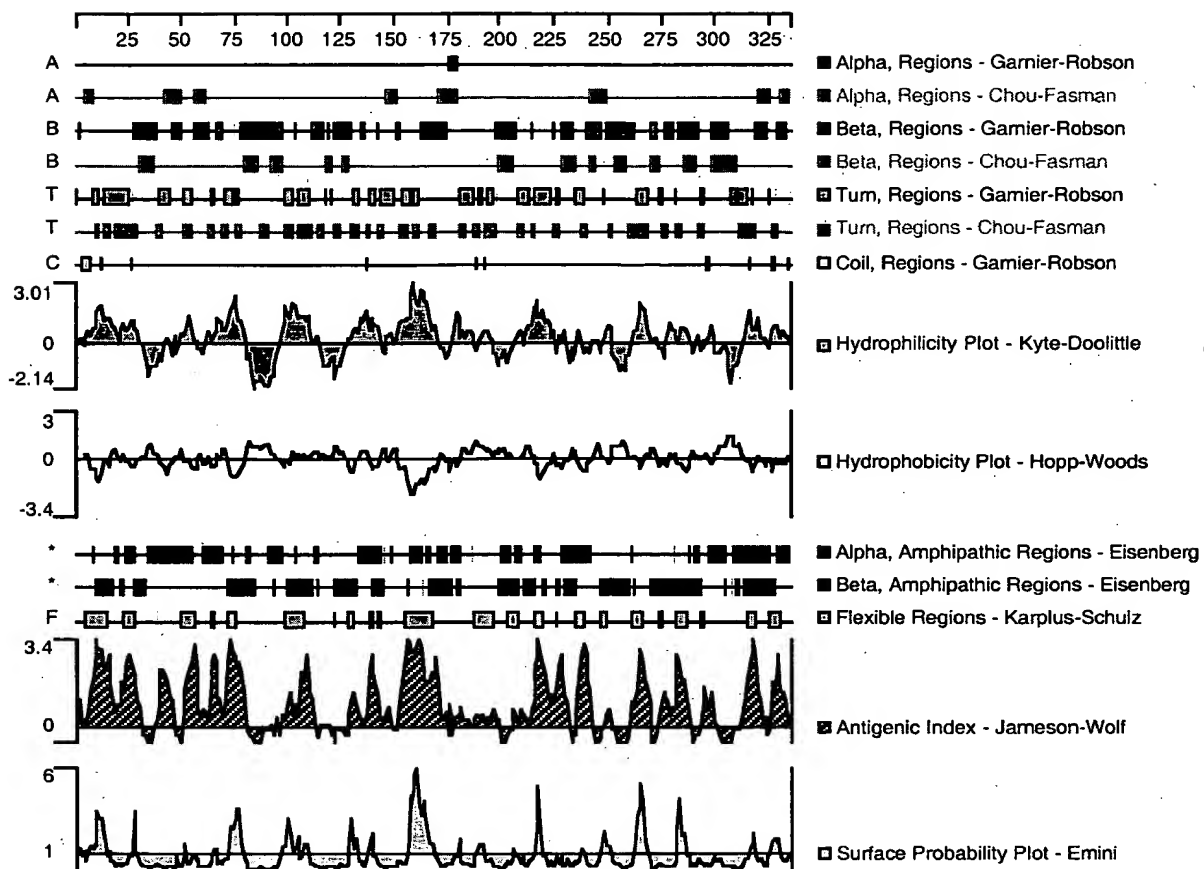


Figure 4

